

SEQUENCE LISTING

<110> Wong, Justin
Winter, Jill
Lalehzadeh, Guita
Warne, Robert

<120> Compositions and Methods of Therapy for
Cancers Characterized by Expression of the Tumor-Associated
Antigen MN/CA IX

<130> PP19155.003

<150> 60/405,577
<151> 2002-08-23

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1380
<212> DNA
<213> Homo

<220>
<221> CDS
<222> (1)...(1380)

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Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
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cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg ctg ctt ctg 96
Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu
20 25 30

atg cct gtc cat ccc cag agg ttg ccc cg^g atg cag gag gat tcc ccc 144
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
35 40 45

ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc gag gag gat 192
 Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
 50 55 60

ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca ccc gga gag 240
 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
 65 70 75 80

gag gat cta cct gga gag gag gat cta cct gga gag gag gat cta cct 288
Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
85 90 95

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gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag tta gag gat 336
Glu Val Lys Pro Lys Ser Glu Glu Gly Ser Leu Lys Leu Glu Asp
          100           105           110

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ctt ccc act gtt gag gct cct gga gat cct caa gaa ccc cag aat aat 384
 Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
 115 120 125

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gcc cac agg gac aaa gaa ggg gat gac cag agt cat tgg cgc tat gga      432
Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly
    130          135          140

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ggc gac ccg ccc tgg ccc cggtgc tcc cca gcc tgc gcg ggc cgc ttc Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe 145 150 155 160	480
cag tcc ccg gtg gat atc cgc ccc cag ctc gcc gcc ttc tgc ccc gcc Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala 165 170 175	528
ctg cgc ccc ctg gaa ctc ctg ggc ttc cag ctc ccg ccc ctc cca gaa Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu 180 185 190	576
ctg cgc ctg cgc aac aat ggc cac agt gtg caa ctg acc ctc cct cct Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro 195 200 205	624
ggg cta gag atg gct ctg ggt ccc ggg cggtac ccgg gct ctg cag Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln 210 215 220	672
ctg cat ctg cac tgg ggg gct gca ggt cgt ccg ggc tcg gag cac act Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr 225 230 235 240	720
gtg gaa ggc cac cgt ttc cct gcc gag atc cac gtg gtt cac ctc agc Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser 245 250 255	768
acc gcc ttt gcc aga gtt gac gag gcc ttggggccg gga ggc ctg Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu 260 265 270	816
gcc gtg ttg gcc gcc ttt ctg gag gag ggc ccg gaa gaa aac agt gcc Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala 275 280 285	864
tat gag cag ttg ctg tct cgc ttg gaa gaa atc gct gag gaa ggc tca Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser 290 295 300	912
gag act cag gtc cca gga ctg gac ata tct gca ctc ctg ccc tct gac Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp 305 310 315 320	960
ttc agc cgc tac ttc caa tat gag ggg tct ctg act aca ccg ccc tgt Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys 325 330 335	1008
gcc cag ggt gtc atc tgg act gtg ttt aac cag aca gtg atg ctg agt Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser 340 345 350	1056
gct aag cag ctc cac acc ctc tct gac acc ctg ttgg gga cct ggt gac Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp 355 360 365	1104
tct cgg cta cag ctg aac ttc cga gcg acg cag cct ttg aat ggg cga Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg 370 375 380	1152
gtg att gag gcc tcc ttc cct gct gga gtg gac agc agt cct cgg gct Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala 385 390 395 400	1200

gct gag cca gtc cag ctg aat tcc tgc ctg gct gct ggt gac atc cta 1248
 Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu
 405 410 415

gcc ctg gtt ttt ggc ctc ctt ttt gct gtc acc agc gtc gcg ttc ctt 1296
 Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu
 420 425 430

gtg cag atg aga agg cag cac aga agg gga acc aaa ggg ggt gtg agc 1344
 Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser
 435 440 445

tac cgc cca gca gag gta gcc gag act gga gcc tag 1380
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 <213> Homo sapiens

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 Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
 35 40 45
 Leu Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
 50 55 60
 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
 65 70 75 80
 Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Asp Leu Pro
 85 90 95
 Glu Val Lys Pro Lys Ser Glu Glu Gly Ser Leu Lys Leu Glu Asp
 100 105 110
 Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
 115 120 125
 Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly
 130 135 140
 Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe
 145 150 155 160
 Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala
 165 170 175
 Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu
 180 185 190
 Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro
 195 200 205
 Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln
 210 215 220
 Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr
 225 230 235 240
 Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser
 245 250 255
 Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu
 260 265 270
 Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala
 275 280 285
 Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser
 290 295 300
 Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp
 305 310 315 320
 Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys
 325 330 335
 Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser

340	345	350
Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp		
355	360	365
Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg		
370	375	380
Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala		
385	390	395
Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu		
405	410	415
Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu		
420	425	430
Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser		
435	440	445
Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala		
450	455	

<210> 3
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for human CA IX proteoglycan
domain construct
<221> CDS
<222> (1)...(540)

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Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala		
1	5	10
		15
ctt gct cca ggc ctc act gtg caa ctg ctg tca ctg ctg ctt ctg		96
Leu Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu		
20	25	30
atg cct gtc cat ccc cag agg ttg ccc cggt atg cag gag gat tcc ccc		144
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro		
35	40	45
ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc gag gag gat		192
Leu Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp		
50	55	60
ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca ccc gga gag		240
Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu		
65	70	75
		80
gag gat cta cct gga gag gag gat cta cct gga gag gag gat cta cct		288
Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro		
85	90	95
gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag tta gag gat		336
Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp		
100	105	110
cta cct act gtt gag gct cct gga gat cct caa gaa ccc cag aat aat		384
Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn		
115	120	125
gcc cat agg agc tcg agc atc cta gcc ctg gtt ttt ggc ctc ctt ttt		432

Ala His Arg Ser Ser Ser Ile Leu Ala Leu Val Phe Gly Leu Leu Phe			
130	135	140	
gct gtc acc agc gtc gcg ttc ctt gtg cag atg aga agg cag cac aga		480	
Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln His Arg			
145	150	155	160
agg gga acc aaa ggg ggt gtg agc tac cgc cca gca gag gta gcc gag		528	
Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val Ala Glu			
165	170	175	
act gga gcc tag		540	
Thr Gly Ala *			

<210> 4
<211> 179
<212> PRT
<213> Artificial Sequence

<220>

<223> Polypeptide encoded by coding sequence for human
CA IX proteoglycan domain construct

<400> 4			
Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala			
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Leu Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu			
20	25	30	
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro			
35	40	45	
Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp			
50	55	60	
Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu			
65	70	75	80
Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro			
85	90	95	
Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp			
100	105	110	
Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn			
115	120	125	
Ala His Arg Ser Ser Ser Ile Leu Ala Leu Val Phe Gly Leu Leu Phe			
130	135	140	
Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln His Arg			
145	150	155	160
Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val Ala Glu			
165	170	175	
Thr Gly Ala			

<210> 5
<211> 1089
<212> DNA
<213> Artificial Sequence

<220>

<223> Coding sequence for human CA IX carbonic anhydrase
domain construct

<221> CDS

<222> (1)...(1089)

<400> 5

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cct gct cca ggc ctc act gtg caa ctg ctg tca ctg ctg ctt ctg Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Ser Leu Leu Leu Leu 20 25 30	96
atg cct gtc cat ccc ggg gat gac cag agt cat tgg cgc tat gga ggc Met Pro Val His Pro Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly 35 40 45	144
gac ccg ccc tgg ccc cgg gtg tcc cca gcc tgc gcg ggc cgc ttc cag Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln 50 55 60	192
tcc ccg gtg gat atc cgc ccc cag ctc gcc gcc ttc tgc ccg gcc ctg Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu 65 70 75 80	240
cgc ccc ctg gaa ctc ctg ggc ttc cag ctc ccg ccg ctc cca gaa ctg Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu 85 90 95	288
cgc ctg cgc aac aat ggc cac agt gtg caa ctg acc ctg cct cct ggg Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly 100 105 110	336
cta gag atg gct ctg ggt ccc ggg cgg gag tac cgg gct ctg cag ctg Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu 115 120 125	384
cat ctg cac tgg ggg gct gca ggt cgt ccg ggc tcg gag cac act gtg His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val 130 135 140	432
gaa ggc cac cgt ttc cct gcc gag atc cac gtg gtt cac ctc agc acc Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr 145 150 155 160	480
gcc ttt gcc aga gtt gag gag gcc ttg ggg cgc ccg gga ggc ctg gcc Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala 165 170 175	528
gtg ttg gcc gcc ttt ctg gag gag ggc ccg gaa gaa aac agt gcc tat Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr 180 185 190	576
gag cag ttg ctg tct cgc ttg gaa gaa atc gct gag gaa ggc tca gag Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu 195 200 205	624
act cag gtc cca gga ctg gac ata tct gca ctc ctg ccc tct gac ttc Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe 210 215 220	672
agc cgc tac ttc caa tat gag ggg tct ctg act aca ccg ccc tgt gcc Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala 225 230 235 240	720
cag ggt gtc atc tgg act gtg ttt aac cag aca gtg atg ctg agt gct Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala 245 250 255	768

aag cag ctc cac acc ctc tct gac acc ctg tgg gga cct ggt gac tct	816
Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser	
260	265
	270

cgg cta cag ctg aac ttc cga gcg acg cag cct ttg aat ggg cga gtg	864
Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val	
275	280
	285

att gag gcc tcc ttc cct gct gga gtg gac agc agt cct cgg gct gct	912
Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala	
290	295
	300

gag cca gtc cag ctg aat tcc tgc ctg gct gct ggt gac atc cta gcc	960
Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala	
305	310
	315
	320

ctg gtt ttt ggc ctc ctt ttt gct gtc acc agc gtc gcg ttc ctt gtg	1008
Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val	
325	330
	335

cag atg aga agg cag cac aga agg gga acc aaa ggg ggt gtg agc tac	1056
Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr	
340	345
	350

cgc cca gca gag gta gcc gag act gga gcc tag	1089
Arg Pro Ala Glu Val Ala Glu Thr Gly Ala *	
355	360

<210> 6

<211> 362

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide encoded by coding sequence for human
CA IX carbonic anhydrase domain construct

<400> 6

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Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu	
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	30
Met Pro Val His Pro Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly	
35	40
	45
Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln	
50	55
	60
Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu	
65	70
	75
Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu	
85	90
	95
Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly	
100	105
	110
Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu	
115	120
	125
His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val	
130	135
	140
Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr	
145	150
	155
Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala	
165	170
	175
Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr	
180	185
	190
Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu	
195	200
	205

Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe
 210 215 220
 Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala
 225 230 235 240
 Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala
 245 250 255
 Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser
 260 265 270
 Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val
 275 280 285
 Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala
 290 295 300
 Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala
 305 310 315 320
 Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val
 325 330 335
 Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr
 340 345 350
 Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
 355 360

<210> 7

<211> 978

<212> DNA

<213> Artificial Sequence

<220>

<223> Coding sequence for glu-tagged human CA IX
carbonic anhydrase domain construct

<221> CDS

<222> (1)...(978)

<400> 7

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1														15		

cct	gct	cca	ggc	ctc	act	gtg	caa	ctg	ctg	tca	ctg	ctg	ctt	ctg	96
Pro	Ala	Pro	Gly	Ieu	Thr	Val	Gln	Ieu	Ieu	Leu	Ser	Leu	Leu	Leu	
20														30	

atg	cct	gtc	cat	ccc	cag	agg	ttg	ccc	cg	atg	cag	gag	gct	agc	gaa	144
Met	Pro	Val	His	Pro	Gln	Arg	Leu	Pro	Arg	Met	Gln	Glu	Ala	Ser	Glu	
35														45		

tac	atg	cca	atg	gaa	caa	gaa	ccc	cag	aat	aat	gcc	cac	agg	gac	aaa	192
Tyr	Met	Pro	Met	Glu	Gln	Glu	Pro	Gln	Asn	Asn	Ala	His	Arg	Asp	Lys	
50														60		

gaa	ggg	gat	gac	cag	agt	cat	tgg	cgc	tat	gga	ggc	gac	ccg	ccc	tgg	240
Glu	Gly	Asp	Asp	Gln	Ser	His	Trp	Arg	Tyr	Gly	Gly	Asp	Pro	Pro	Trp	
65														80		

ccc	cg	gt	tcc	cca	gcc	tgc	g	gc	tc	c	tg	cc	gt	g	at	288
Pro	Arg	Val	Ser	Pro	Ala	Cys	Ala	Gly	Arg	Phe	Gln	Ser	Pro	Val	Asp	
85														95		

atc	cgc	ccc	cag	ctc	gcc	ttc	tgc	ccg	gcc	ctg	cgc	ccc	ctg	gaa	336
Ile	Arg	Pro	Gln	Leu	Ala	Ala	Phe	Cys	Pro	Ala	Leu	Arg	Pro	Leu	Glu
100														110	

ctc	ctg	ggc	ttc	cag	ctc	ccg	ccg	ctc	cca	gaa	ctg	cgc	ctg	cgc	aac	384
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Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn			
115	120	125	
aat ggc cac agt gtg caa ctg acc ctg cct cct ggg cta gag atg gct			432
Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala			
130	135	140	
ctg ggt ccc ggg cgg gag tac cgg gct ctg cag ctg cat ctg cac tgg			480
Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp			
145	150	155	160
ggg gct gca ggt cgt ccg ggc tcg gag cac act gtg gaa ggc cac cgt			528
Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg			
165	170	175	
ttc cct gcc gag atc cac gtg gtt cac ctc agc acc gcc ttt gcc aga			576
Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg			
180	185	190	
gtt gac gag gcc ttg ggg cgc ccg gga ggc ctg gcc gtg ttg gcc gcc			624
Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala			
195	200	205	
ttt ctg gag gag ggc ccg gaa gaa aac agt gcc tat gag ctc cac acc			672
Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Leu His Thr			
210	215	220	
ctc tct gac acc ctg tgg gga cct ggt gac tct cgg cta cag ctg aac			720
Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn			
225	230	235	240
ttc cga gcg acg cag cct ttg aat ggg cga gtg att gag gcc tcc ttc			768
Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe			
245	250	255	
cct gct gga gtg gac agc agt cct cgg gct gct gag cca gtc cag ctg			816
Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln Leu			
260	265	270	
aat tcc tgc ctg gct gct ggt gac atc cta gcc ctg gtt ttt ggc ctc			864
Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala Leu Val Phe Gly Leu			
275	280	285	
ctt ttt gct gtc acc agc gtc gcg ttc ctt gtg cag atg aga agg cag			912
Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln			
290	295	300	
cac aga agg gga acc aaa ggg ggt gtg agc tac cgc cca gca gag gta			960
His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val			
305	310	315	320
gcc gag act gga gcc tag			978
Ala Glu Thr Gly Ala *			
325			

<210> 8
<211> 325
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide encoded by coding sequence for
glu-tagged human CA IX carbonic anhydrase domain
construct

<400> 8

Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
 1 5 10 15
 Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu
 20 25 30
 Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Ala Ser Glu
 35 40 45
 Tyr Met Pro Met Glu Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys
 50 55 60
 Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp
 65 70 75 80
 Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp
 85 90 95
 Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu
 100 105 110
 Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn
 115 120 125
 Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala
 130 135 140
 Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp
 145 150 155 160
 Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg
 165 170 175
 Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg
 180 185 190
 Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala
 195 200 205
 Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Leu His Thr
 210 215 220
 Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn
 225 230 235 240
 Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe
 245 250 255
 Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln Leu
 260 265 270
 Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala Leu Val Phe Gly Leu
 275 280 285
 Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln
 290 295 300
 His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val
 305 310 315 320
 Ala Glu Thr Gly Ala
 325

<210> 9

<211> 978

<212> DNA

<213> Artificial Sequence

<220>

<223> Coding sequence for glu-tagged mutant human CA IX
 carbonic anhydrase domain construct

<221> CDS

<222> (1)...(978)

<400> 9

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 Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
 1 5 10 15

cct gct cca ggc ctc act gtg caa ctg ctg tca ctg ctg ctt ctg 96
 Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu

20	25	30	
atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag gct agc gaa Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Ala Ser Glu	35	40	144
		45	
tac atg cca atg gaa caa gaa ccc cag aat aat gcc cac agg gac aaa Tyr Met Pro Met Glu Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys	50	55	192
		60	
gaa ggg gat gac cag agt cat tgg cgc tat gga ggc gac ccc tgg Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp	65	70	240
		75	
ccc cgg gtg tcc cca gcc tgc gcg ggc cgc ttc cag tcc ccc gtg gat Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp	85	90	288
		95	
atc cgc ccc cag ctc gcc ttc tgc ccg gcc ctg cgc ccc ctg gaa Ile Arg Pro Gln Leu Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu	100	105	336
		110	
ctc ctg ggc ttc cag ctc ccg ccg ctc cca gaa ctg cgc ctg cgc aac Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn	115	120	384
		125	
aat ggc cac agt gtg caa ctg acc ctg cct cct ggg ota gag atg gct Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala	130	135	432
		140	
ctg ggt ccc ggg cgg gag tac cgg gct ctg cag ctg caa ctg cag tgg Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu Gln Leu Gln Trp	145	150	480
		155	
160			
ggg gct gca ggt cgt ccg ggc tcg gag cac act gtg gaa ggc cac cgt Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg	165	170	528
		175	
ttc cct gcc gag atc caa gtg gtt cac ctc agc acc gcc ttt gcc aga Phe Pro Ala Glu Ile Gln Val Val His Leu Ser Thr Ala Phe Ala Arg	180	185	576
		190	
gtt gac gag gcc ttg ggg cgc ccg gga ggc ctg gcc gtg ttg gcc gcc Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala	195	200	624
		205	
ttt ctg gag gag ggc ccg gaa gaa aac agt gcc tat gag ctc cac acc Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Leu His Thr	210	215	672
		220	
ctc tct gac acc ctc tgg gga cct ggt gac tct cgg cta cag ctg aac Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn	225	230	720
		235	
240			
ttc cga gcg acg cag cct ttg aat ggg cga gtg att gag gcc tcc ttc Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe	245	250	768
		255	
cct gct gga gtg gac agc agt cct cgg gct gct gag cca gtc cag ctg Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln Leu	260	265	816
		270	
aat tcc tgc ctg gct gct ggt gac atc cta gcc ctg gtt ttt ggc ctc Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala Leu Val Phe Gly Leu	275	280	864
		285	

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ctt ttt gct gtc acc agc gtc gcg ttc ctt gtg cag atg aga agg cag 912
Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln
         290          295          300

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cac aga agg gga acc aaa ggg ggt gtg agc tac cgc cca gca gag gta 960
 His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val
 305 310 315 320

gcc gag act gga gcc tag
Ala Glu Thr Gly Ala *
325

<210> 10
<211> 325
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide encoded by coding sequence for
glu-tagged mutant human CA IX carbonic anhydrase
domain construct